

## **REMARKS**

Upon entry of the foregoing amendments, claims 1–4, 10–14, 16, 18, 19, 25 and 26 are pending. Applicants have amended claims 3 and 4 to correct antecedent basis. Thus, claims 3 and 4 now recite “polynucleotides.” Basis for these amendments can be found in the specification as originally filed, and in particular, in originally filed claims 1 and 2. Applicants have amended claim 13 to correct improper dependency. Thus, claim 13 now recites “the host cell of claim 12.” Applicants have amended claim 19 to correct clerical errors and improper dependency. Thus, claim 19 now recites “the vaccine vector of claim 16.” Applicants have amended claim 25 to correct clerical errors. Applicants have added new claims 38 and 39 to more accurately claim the present invention. New claims 38 and 39 further limit the type of host cells to be used in the present invention. Specifically, new claims 38 and 39 are directed to mammalian cells and human cells respectively. Basis for these amendments can be found in the specification as originally filed, and in particular, at pg. 14, lines 9–14; pg. 15, line 31; and in originally filed claim 17.

These amendments add no new matter.

### ***Co-Pending Applications***

Applicants acknowledge the Examiner’s request regarding copies of claims, correlated with the serial number of the case in which they appear, for each pending application directed to the pending subject matter.

Applicants respectfully submit that acquiescing to the Examiner’s request of providing copies of pending claims would be unduly onerous and expensive for Applicants. Applicants have **no obligation to provide the Examiner with copies of claims in any pending applications.** In fact, Applicants submit that, under M.P.E.P. §804, it is the Examiner’s burden to identify any potential statutory and/or “obvious-type” double patenting rejections. *See,* M.P.E.P. §804(I)(B), which states:

Occasionally, the examiner becomes aware of two copending applications filed by the same inventive entity, or by different inventive entities having a common

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inventor, and/or that are filed by a common assignee that would raise an issue of double patenting if one of the applications became a patent.

However, Applicants agree to provide the Examiner copies of the requested claims upon determination of allowable subject matter in the present application.

### ***Drawings***

Applicants acknowledge the Draftsperson's objection to the Drawings filed in the present application.

Applicants will provide formal drawings upon determination of allowable subject matter in the present application.

### ***Oath/Declaration***

Applicants acknowledge the Examiner's objection to the Declaration as filed in the present application. Applicants have enclosed herewith an executed Declaration. Accordingly, Applicants believe that the present objection is now moot.

### ***Specification***

The Examiner has objected to the Specification as having various informalities.

Applicants have amended the Specification to correct these informalities. Accordingly, Applicants believe that the present objection is now moot.

### ***Provisional Double Patenting Rejection over Co-pending Applications***

The Examiner has provisionally rejected claims 1–4, 10–14, 16–19, 25 and 26 under 35 U.S.C. §101 as claiming the same invention as that of claims 1, 20, 21, 25–28, 32–35, 41 and 42 of co-pending application U.S.S.N. 09/376,770 ("770").

Applicants traverse. 37 CFR §1.78(b) provides that when two or more applications filed by the same Applicant contain conflicting claims, elimination of such claims from all but one application may be required in the absence of good and sufficient reason for their retention

during pendency in more than one application. However, the M.P.E.P. clearly states that “[t]his paragraph is appropriate only when the conflicting claims are **patentably distinct**. See MPEP §822. *See also*, In re Zickendraht, 319 F.2d 225, 138 USPQ 22 (CCPA 1963) (where the Court held that the doctrine is well established in that claims in different applications need be more than merely different in form or content and that **patentable distinction must exist to entitle applicants to a second patent**).

The ‘770 application is a co-pending application having the both the same inventive entity and assignee. However, both applications are directed to distinct sequences encoding *different Chlamydia* polypeptides. Applicants have attached herewith an alignment comparison between the polypeptide of the present application with those disclosed by U.S.S.N. 09/376,770 (Exhibits A and B). The comparisons clearly show that the polypeptides according to the present invention are **completely different** from those disclosed in the ‘770 application.

Accordingly, in light of the arguments above, Applicants respectfully request reconsideration and withdrawal of the present provisional double patenting rejection.

### ***35 U.S.C. §112, First Paragraph Rejections***

The Examiner has rejected claims 1–4, 10–14, 16–19, 25 and 26 under 35 U.S.C. §112, first paragraph as containing subject matter which was not described in the Specification in such a way as to enable one skilled in the art to make and/or use the invention, stating that the Specification is not enabled for a polynucleotide encoding a polypeptide having a sequence that is “at least 75% homologous” to SEQ ID NO:2 and “functional fragments thereof.” Specifically, the Examiner has alleged that:

Without a clear and unambiguous description of how to perform the comparison, the scope of the claims can not be envisaged (*sic*). Without a specific disclosure of the parametric values used in the algorithm, the sequence identity between two sequences has no common meaning within the art and therefore, one of ordinary skill in the art cannot be sure of the sequences embraced by the claims and would not be able to make and use those polynucleotide or polypeptide sequence homologs as recited in the instant claims, without undue experimentation.

*See e.g.*, December 13, 2000 Office action at pg. 5.

Applicants traverse. Methods and computational programs for conducting sequence comparisons for homology are well known within the art. Homology is typically measured using **sequence analysis software** (*e.g.*, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). Similar amino acid sequences are aligned to obtain the maximum degree of homology (*i.e.*, identity). To this end, it may be necessary to artificially introduce gaps into the sequence. Once the optimal alignment has been set up, the degree of homology (*i.e.*, identity) is established by recording all of the positions in which the amino acids of both sequences are identical, relative to the total number of positions.

The Specification also describes a preferred method for determining amino acid similarities, including amino acid sequence homology:

One particularly preferred method of determining amino acid similarities is the PAM25O matrix described in Dayhoff *et al.*, 5 ATLAS OF PROTEIN SEQUENCE AND STRUCTURE 345-352 (1978 & Supp.), incorporated by reference herein. A similarity score is first calculated as the sum of the aligned pairwise amino acid similarity scores. Insertions and deletions are ignored for the purposes of percent homology and identity. Accordingly, gap penalties are not used in this calculation. The raw score is then normalized by dividing it by the geometric mean of the scores of the candidate compound and the reference sequence. The geometric mean is the square root of the product of these scores. The normalized raw score is the percent homology.

*See e.g.*, Specification at pg. 9, lines 15–23. Furthermore, the Specification specifically and clearly defines a "homologous amino acid sequence" as:

an amino acid sequence that differs from an amino acid sequence shown in SEQ ID NO: 2, only by one or more conservative amino acid substitutions, or by one or more non-conservative amino acid substitutions, deletions, or additions located at positions at which they do not destroy the specific antigenicity of the polypeptide. Preferably, such a sequence is at least 75%, more preferably 80%, and most preferably 90% identical to an amino acid sequence shown in SEQ ID NO: 2. Homologous amino acid sequences include sequences that are identical or substantially identical to an amino acid sequence as shown in SEQ ID NO: 2.

*Id* at pg. 8, lines 21–29. The Specification also describes amino acid sequence identity and conservative substitutions as:

By "amino acid sequence substantially identical" is meant a sequence that is at least 90%, preferably 95%, more preferably 97%, and most preferably 99% identical to an amino acid sequence of reference and that preferably differs from the sequence of reference, if at all, by a majority of conservative amino acid substitutions. Conservative amino acid substitutions typically include substitutions among amino acids of the same class. These classes include, for example, (a) amino acids having uncharged polar side chains, such as asparagine, glutamine, serine, threonine, and tyrosine; (b) amino acids having basic side chains, such as lysine, arginine, and histidine; (c) amino acids having acidic side chains, such as aspartic acid and glutamic acid; and (d) amino acids having nonpolar side chains, such as glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and cysteine.

*Id* at pg. 9, lines 8–14. Thus, Applicants assert that one of ordinary skill in the art could make and use such homologous sequences in, for example, vaccines and diagnostic reagents. Accordingly, Applicants respectfully request reconsideration and withdrawal of the present rejection.

### ***35 U.S.C. §112, Second Paragraph Rejections***

The Examiner has rejected claims 3, 4, 13, 17 and 19 under 35 U.S.C. §112, second paragraph, as being indefinite for improper antecedent basis.

Applicants have amended claims 3 and 4 to correct antecedent basis. Thus, claims 3 and 4 now recite "polynucleotides." Basis for these amendments can be found in the specification as originally filed, and in particular, in originally filed claims 1 and 2. Applicants have amended claim 13 to correct improper dependency. Thus, claim 13 now recites "the host cell of claim 12." Applicants have amended claim 19 to correct improper dependency. Thus, claim 19 now recites "the vaccine vector of claim 16." Applicants have added new claims 38 and 39 to more accurately claim the present invention. New claims 38 and 39 further limit the type of host cells to be used in the present invention. Specifically, new claims 38 and 39 are directed to mammalian cells and human cells respectively. Basis for these amendments can be found in the specification as originally filed, and in particular, at pg. 14, lines 9–14; pg. 15, line 31; and in originally filed claim 17.

In light of the above amendments, Applicants believe that the present rejections are now moot. Accordingly, Applicants respectfully request reconsideration and withdrawal of the present rejections.

**35 U.S.C. §102 Rejection**

The Examiner has rejected claims 1–4, 10–13, 16–19, 25 and 26 under 35 U.S.C. §102(b) as being anticipated by Longbottom *et al.* (**Longbottom**). Specifically, the Examiner has stated that **Longbottom** teaches “*chlamydial* genes or sequences coding for highly immunogenic protein fragments comprising 8 or 9 amino acid residues.”

Applicants traverse. **Anticipation requires the disclosure in a single prior art reference of each element of the claim under consideration.** *W.L. Gore & Associates v. Garlock, Inc.*, 220 USPQ 303, 313 (Fed. Cir. 1983), *cert. denied*, 469 U.S. 851 (1984); *Connell v. Sears Roebuck & Co.*, 220 USPQ 193, 198 (Fed. Cir. 1983); *Verdegaal Bros. v. Union Oil Co. of California*, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987); *In re Spada*, 15 USPQ2d 1655 (Fed. Cir. 1990); MPEP § 2131. **“There must be no difference between the claimed invention and the reference disclosure, as viewed by a person of ordinary skill in the field of the invention.”** *Scripps Clinic & Research Foundation v. Genentech Inc.*, 18 USPQ 2d 1001, 1010 (Fed. Cir. 1991).

Although both applications are directed to *Chlamydia* polypeptides, **Longbottom** discloses distinct sequences encoding *different Chlamydia* polypeptides. Applicants have attached herewith an alignment comparison between the polypeptides of the present application with those disclosed by **Longbottom** (Exhibit C1 to C4). Applicants have highlighted the regions that the Examiner has suggested would be identical between the present application and **Longbottom**. As can be seen by the highlighted regions, the rejection seems to be based upon that of identical fragments within the polynucleotides and/or polypeptides of the present invention, **not on the entire polynucleotide or polypeptide**. Furthermore, the comparisons clearly show that the polynucleotides and polypeptides according to the present invention are, in

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fact, **different** from those disclosed in **Longbottom**. Thus, Applicants assert that the present application is not anticipated by **Longbottom**.

Accordingly, in light of the arguments above, Applicants respectfully request reconsideration and withdrawal of the present rejection.

## CONCLUSION

On the basis of the foregoing amendments and remarks, Applicants respectfully submit that the pending claims are in condition for allowance. If there are any questions regarding these amendments and remarks, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,



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Dated: December 4, 2001

## VERSION WITH MARKINGS TO SHOW CHANGES MADE

### *In the Specification:*

The paragraph beginning at line 6, pg. 8 was amended as follows:

-- [FIG. 1] FIG. 1A to 1I shows the nucleotide sequence (top sequence) and the deduced amino acid sequence (bottom sequence) of the full length *98 kDa putative outer membrane protein* gene (SEQ ID NO: 1) and the processed sequence from *Chlamydia pneumoniae* (SEQ ID NO: 2). --

The paragraph beginning at line 9, pg. 8 was amended as follows:

-- [FIG. 2] FIG. 2A to 2H shows the restriction enzyme analysis of nucleotide sequence encoding the *C. pneumoniae* *98 kDa putative outer membrane protein* gene. --

The paragraph beginning at line 13, pg. 16 was amended as follows:

A recombinant expression system can be selected from prokaryotic and eukaryotic hosts. Eukaryotic hosts include yeast cells (*e.g.*, *Saccharomyces cerevisiae* or *Pichia pastoris*), mammalian cells (*e.g.*, COS1, NIH3T3, or JEG3 cells), arthropods cells (*e.g.*, *Spodoptera frugiperda* (SF9) cells), and plant cells. Preferably, a prokaryotic host such as *E. coli* is used. Bacterial and eukaryotic cells are available from a number of different sources to those skilled in the art, *e.g.*, the American Type Culture Collection [(ATCC; Rockville, Maryland)] (ATCC; 10801 University Boulevard, Manassas, VA 20110-2209).

### *In the Claims:*

3. (Amended) The polynucleotide of claim 2 wherein the fusion polypeptide is a heterologous signal peptide.

4. (Amended) The polynucleotide of claim 2 wherein the polynucleotide encodes a functional fragment of the polypeptide having the SEQ ID NO: 2.
13. (Amended) The host cell of claim 12[0], wherein said host cell is a prokaryotic cell.
19. (Amended) A pharmaceutical composition, comprising an immunologically effective amount of the vaccine vector of claim 16[4].
25. (Amended) A polynucleotide probe reagent capable of detecting the presence of *Chlamydia* in a biological material, comprising a polynucleotide that hybridizes to the polynucleotide of claim 1 under stringent conditions.
- 38. (New) The host cell of claim 14, wherein said eukaryotic cell is a mammalian cell.
39. (New) The host cell of claim 38, wherein said mammalian cell is a human cell.--

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## EXHIBIT C - The Alignment of LONGBOTTOM to CPN 100396 (SEQ ID NO:1)

### Alignment 1

GAP of: cpu72499.seq check: 4475 from: 1 to: 4926

WPDEF Chlamydophila abortus putative outer membrane protein gene, partial  
LOCUS CPU72499 4926 bp DNA BCT 13-MAY-1999  
DEFINITION Chlamydophila abortus putative outer membrane protein gene, partial  
cds; and putative 98 kDa outer membrane protein gene, complete cds.  
ACCESSION U72499  
VERSION U72499.1 GI:1657776 . . .

to: cpn100396.seq check: 452 from: 1 to: 3000

WPDEF  
cpn100396

Symbol comparison table: /big1/gcg/gcgccore/data/rundata/nwsgapdna.cmp  
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000  
Length Weight: 3 Average Mismatch: 0.000

Quality: 14521 Length: 5027  
Ratio: 4.840 Gaps: 13  
Percent Similarity: 53.087 Percent Identity: 53.087

Match display thresholds for the alignment(s):  
| = IDENTITY  
: = 5  
. = 1

cpu72499.seq x cpn100396.seq March 2, 2001 11:29 ..

1951 CAAGCAGTCCTCTCTAGAACGCAGGGGCCTTTACCAAAATGACAAAAA 2000

1 ..... cgctct 6

2001 CATGTCAAGTCTTCTGTATTAGACTTGCTTCTTGTATCTTGAGT 2050

7 taccttagtagaggtgagtgaatttcttgacttgttctctatgggtgt 56

2051 ATTTAACGAAACTGTTTTTCATTCACCACA.AGTGTATAAAATGAGG 2099

57 atctctaaaatattaaattcaaatcaaagtatatatttacaatgaag 106

2100 CCTTCTTTATATAAGATTTAATATCGTCGACGCTGACGTTACCAATATC 2149

107 tcttccttcccaagttgtatattctacatggctatcccttgc 156

150 TTTTCACCTCTCGCAATTGCATGCAGAAGTGGCTTAACCAAGAACATCTA 2199  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
157 tatgattgtac.....cgagacagtttggattcaagtgcgagttcg 200

2200 TTCTCGATGCAAATGGAGCATTCAAGTCCGCAATCTACAAGCACTGCAGGG 2249  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
201 atgggaataaaaaatggtaattttcagttcgtgagagtcaaggaagatgct 250

2250 GGAACGATTTACAACGTCGAGAGTGATATTCTATTGTAGATGTAGGACA 2299  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
251 ggaactacctacctatTTAaggaaatgtcaactctagaaaatattccctgg 300

2300 GACAG...CGGCTCTTGCTTCCTCAGCTTGTTCAGACTGCAGACAAACC 2346  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
301 aacaggcacagcaatoacaaaaaagctgtttaaacaacactaaggcgatt 350

2347 TAACTTTCAAAGGGAAACAACCATAGCTTATCCATAACGAACGCGAATGCC 2396  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
351 tgactttcacaggtAACGGGAactctcttatTTGTTCCAACCGGTGGATGCA 400

2397 GGAGCTAATCC...TGCAGGAAATTAAACGTTAACACTGCCGATAAGATTCT 2443  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
401 gggactgttagcaggggctgttaacagcagcagcgtggtagataaatctac 450

2444 TACGCTGACAGATTCTAAGTTGAGCTTAAGGAATGCCCATCTTCTC 2493  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
451 cacgttatagggtttcttcgtatctttattgcgtctccctggaaagtt 500

2494 TAGTGAATACTGGAAAAGGGG...TATGAAATCCGGAGGAGCATTAAAC 2540  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
501 cgataactaccggcaaaggagccgttagctgctctacggtagcttgagt 550

2541 TTAGCGAATAATGCCAGTATTCTGTTGATCAGAACTATTCCGCTGAGAA 2590  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
551 ttgacaaaaaaaaatgtcagttgtcttcagcaaaaaactttcaacggataa 600

2591 TGGTGGAGCCATCTTGCAGGAACTTTCTTAACCGGCTCGAGCAAAG 2640  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
601 tggcggtgttatcccgcaaaaactttcattaaacaggactacaatgt 650

2641 AAATCAGCTTCACCACAACTCTACTGCGAAAAAAAGGTGGAGCGATTGCT 2690  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
651 cagctctgtttctgaaaataccctcctcaaaagaaaggcgagccattcag 700

2691 GCTACGGGAATAGCTCATCTTCCGACAACCAAGGCACAATCAGATTTC 2740  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
701 acttccgatgcccttaccattactggaaaccaaggaaagtctcttttc 750

2741 TGGGAACACTGCTGTGAATTCTGGGGGAGCAGTATATTCAAGAAGCTTCTA 2790  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
751 tgacaataacttctcgattctggagctgcaattttacagaaggcctcg 800

2791 TGACGATTGCAGGTAAACAAACCAACGTTGCTTTAGCAACAAATGCTGTTCC 2840  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
801 tgactattctaataatgctaaagttccttattgacaataaggcata 850

2841 GG.....TTCATCTGATGGTTGCGGTGGAGCTATCCATTG 2875



1545 aacctgctgatactagcaccataaacaattggtcattaacatcagtct 1594  
3561 TTAGATGGGAAAAAAATTGCCGTAGTCGATGCCGTTGCTGGGAAGAA 3610  
1595 atagacggtgcaaagaaggcaaaaatagaaaccaagctacgtcaaaaaa 1644  
3611 TGTGACTTTATCAGGTGCTATTGGCGTTATTGATCCTACAGGGAAAGTTT 3660  
1645 tctgacttatctgaaaccatcactttatggacccgacgggcacgtttt 1694  
3661 ATGAAAACCATAAGCTAAATGATACGTTAGCTTAGGAGGAATTCAACTT 3710  
1695 atgaaaatcatagttaaagaaatcctcagtcctacgacatcttagagctc 1744  
3711 TCTGGGAAAGGTTCGGTGACAACAAACCAACGTCGCCTAGTCATGTTGGG 3760  
1745 aaagcttctggaactgtaacaaggcaccgcagtgactccagatcctataat 1794  
3761 TGTTGCTGAAACCCACTATGGTTATCAAGGAAACTGGTCTGTCAGTTGGG 3810  
1795 gggtgagaaaattccattacggctatcaggga.....acttggg 1832  
3811 TCAAAGATAATAACTCTGATCCTAAAACACAAACAGCAATCTTACCTGG 3860  
1833 gcccaattgtttggggacaggggctctacgactgcaaccttcaactgg 1882  
3861 AATAAAACAGGATATGTTCCAATCCTGAACGTCGTGCTCCGCTAGTACT 3910  
1883 actaaaactggctatattcctaattcccgagcgtatcgctttagtccc 1932  
3911 CAATAGCCTTGGGGATCCTTATAGATTACGTTCTATTCAAGATGTCT 3960  
1933 taatagcttatggaatgcatttatagatattagctctccattatctta 1982  
3961 TGGAACGTAGTGTTGATAGTATTCTTGAGACACGTCGTGGTTGGTC 4010  
1983 tggagactgcaaacgaagggttgc...agggagaccgtgttttgtgt 2029  
4011 TCTGGAATTGGGAACTTCTCCATAAAGATCGGAATGCTGAAAATCGCAA 4060  
2030 gctggattatctaacttcttccataaggatagtacaaaaacacgacgcgg 2079  
4061 ATTCCGTATATCAGTCGGGATATGTGTTAGGAGCCACAACAAATACCT 4110  
2080 gtttcgcatttgagttggcggttatgtcataggagggaaacctacatactt 2129  
4111 CGAGAGAGGATTCTCTTAGTGTGGCTTCTGTCAGTTATTGCAAAAGAT 4160  
2130 gttcagataagattcttagtgctgcatttgcagctttggaaagagat 2179  
4161 AAAGACTACCTTGTAAGCAAGAACGCCAAACGTCTATGCGGGTTCTGT 4210  
2180 agagactactttgttagctaagaatcaaggtagtacagtctacggaggaaactct 2229  
4211 ATATTATCAGCATGTGAGCAAGTTGATGATCTCACGCCGTTATTAATG 4260  
2230 ctattaccagca.....caacgaaacctatatctcttccttgcaaac 2273

4261 GGCCTAACACGTGTTCAAGGGTTCTAAAGAGATTCCTATTCTTG 4310  
 | | | | || | | || | || | || | || | || | || | |  
 2274 tacggcctgttcgttgcctatgttccatcacagagattcctgttcttt 2323  
  
 4311 GATGCACAAATTACCTATTGCCACACGGCCAACAACATGACAACGTCCTA 4360  
 | | | | || | | || | | || | | || | | || | | | |  
 2324 tcaggaaaccttagctacacccatacggataacgatctgaaaaccaagta 2373  
  
 4361 TACAGACTATCCTGAAGTGAAAGGTTCTGGGTAATGATAACCTGGGCT 4410  
 | | | | || | | || | | || | | || | | || | | | |  
 2374 tacaacatatacctactgttaaggaagctggggaatgatagttcgctt 2423  
  
 4411 TAACTTGTCTACTAGCGTACCTATCCCGTATTAGTTCTTCTATCTT 4460  
 | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2424 tagaattcggtgaaagagctccgatttgcttagatgaaagtgcgtctattt 2473  
  
 4461 GATAGTTATGCACCGTTGCAAAATTACAAGTTGTCTATGCGCACCAAGA 4510  
 | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2474 gagcagttacatgcccttcatgaaattgcagttgtctatgcacatcagga 2523  
  
 4511 TGACTTTAAAGAACCAACAAACAGAAGGCCGGTCTTGAAAGCAGCGATC 4560  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2524 aggtttaaagaacacagggAACAGAGCTCGTGAATTGGAAGTAGCCGTC 2573  
  
 4561 TTCTCAACGTTCTGTACCTATAGGTATAAAATTGAGAAACTCTCCTAT 4610  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2574 ttgtgaatcttgccctacctatcggatccgatttgataaggaatcagac 2623  
  
 4611 GGAGAGAGAAGTGCCTATGATCTTACACTGATGTATACCTGATGTGTA 4660  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2624 tgccaagatgcaacgtacaatctaactcttggttatactgtggatcttgt 2673  
  
 4661 CCGTCATAATCCAAGCTGTATGACAGGATTGGCGATCAATGACGTTCCCT 4710  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2674 tcgttagtaaccccgactgtacgacaaacactgcgaattagcggtgattctt 2723  
  
 4711 GGTAAACCACAGCTACGAATCTGCTAGACAAGCTTCATAGTCGCGCG 4760  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2724 gaaaaacccctcggtacgaatttggcaagacaagctttagtcctcgtgca 2773  
  
 4761 GGTAAACCATATTGCCTAACCTCTGGTGTGAGATGTTCAAGTCAGTTGG 4810  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2774 gggaccattttgccttaactcaaatttgaaggccttagccaattttc 2823  
  
 4811 TTTCGAATTACGAAGCTCTCAAGAAATTATAACGTAGATCTGGCGCTA 4860  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2824 ttttgaattgcgtgggtcatctcgcaattacaatgttagacttaggagcaa 2873  
  
 4861 AGGTCGCGTTCTAAAAAGCTCCCCCTGCCAGCTGGGCAGGGTTCTC 4910  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2874 aataccaattctaattgcgttagcttggtaaagagctccatcatcgaag 2923  
  
 4911 CTTATTCTAGTCTAGA..... 4926  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 2924 gaaaaagagctttaagatttgcgttagctttcgatttcgatttcc 2973

## *Alignment 2*

GAP of: cpu65942.seq check: 1642 from: 1 to: 6110

WPDEF Chlamydophila abortus strain S26/3 POMP91A and POMP90A precursor,  
LOCUS CPU65942 6110 bp DNA BCT 07-MAY-1999  
DEFINITION Chlamydophila abortus strain S26/3 POMP91A and POMP90A precursor,  
genes, complete cds.  
ACCESSION U65942  
VERSION U65942.1 GI:1617505 . . .

to: cpn100396.seq check: 452 from: 1 to: 3000

WPDEF  
cpn100396

Symbol comparison table: /big1/gcg/gcgcore/data/rundata/nwsgapdna.cmp  
CompCheck: 8760

Gap Weight: 50 Average Match: 10.000  
 Length Weight: 3 Average Mismatch: 0.000  
 Quality: 13146 Length: 6140  
 Ratio: 4.382 Gaps: 20  
 Percent Similarity: 49.428 Percent Identity: 49.428

```
Match display thresholds for the alignment(s):
    | = IDENTITY
    : = 5
    . = 1
```

cpu65942.seq x cpn100396.seq March 2, 2001 13:39 ..

2251 CTTTAAGGAAAACAATAGCGATCAAGGAAGATACTTGAAAGTAATAACC 2300  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
1 .....cgctcttaccttagtagaggttgagtgaatttctt 34  
  
2301 TCACCAAAC TTATCTATGCCCATAGGTGTGAAATTGGAAAAATTCTCTCAC 2350  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
35 gacttggtttcctattggtgtatctcttaaaatattaaattcaaaaatca 84  
  
2351 AAGGATACCGCTTCTTACAACCTTACCCCTGGCTTATGCTCCAGATATCGT 2400  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
85 aagtatatattttacaatgaagtgcttcccaagttgtatatttcta 134  
  
2401 AAGAAGCAACCTGACTGTACTGCCCTCTCTGTTAGTGAGCCCCAACCTCTG 2450  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
135 catttgc.....tatttcccttggctatgattgctaccgaga 173  
  
2451 CTGTCTGGTAACTAAAGCTAATAACCTTGC CGCGGCATGCTTCATATTA 2500  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
174 cagtttggattcaagtgcgagttcgatggaaataaaaatggtaattt 223

2501 CAAGCAGGAAATTACTTGGCTTAACTCGCAACACGGAGCTCTCAGTC 2550  
224 tcagttcgtagagtcaggaagatgctggaaactacacctac...attta 269  
2551 ATTCGGTTCGAACCTCGAGGTCTGCCGCACCTATAACATAGATCTCG 2600  
270 agggaaaatgtcactctagaaaatattcctggAACAGGcacagcaatcaca 319  
2601 GATCGAAGATCCAGTTCTAATCTCATCCACCTCCCCTGCTCCGTAGACAC 2650  
320 aaaagctg.....tttaacaacactaaggcgatttgactttcacag 362  
2651 GGAGCAGGGCCTCCCTTGTCTACTCTAGCTGGTGACCTTGACTTTAAT 2700  
363 gtaacggaaactctctattgttccaaacgggtggatgcaggactgttagca 412  
2701 TATTTTATGATCGAGTTAGGATATCTCAAATCACCCAAAGCATGAATT 2750  
413 ggggctgctgtt.....aacagcagcgt 435  
2751 ATGAAACATCCAGTCTACTGGTTCTTAATATCCTCGAGCCTATTGCCTC 2800  
436 ggtagataaatctaccacgttatagggtttctcgctatctttattg 485  
2801 GAATTCTTGAGCTTCGCTAACGACGCTCAAACAGCCTTAACCCCTCCG 2850  
486 cgtctcctggaaagttcgataactaccggcaaaggagccgttagctgct 535  
2851 ATAGCTATAATGGAAATGTGACCTCTGAGGAGTTCCAGTAAAAGAAACT 2900  
536 acgggttagcttgagttgaca.....aaaaatgtcagttgc 572  
2901 TCATCAGGAACACGTATACTTGTGAAGGCAATGTGTATCTCCTTGC 2950  
573 tcttcagcaaaaactt....ttcaacggataatggcggtgctatcaccgc 618  
2951 AGGGAAAGATTCAAGGTCTAAAGAAAAAGTTGTTCTCAGCTACTGATAACC 3000  
619 aaaaactcttcattAACAGGGactacaatgtcagctctgtttctgaaa 668  
3001 TTACCTTCCTAGGAAACGGGTATACTCTTGCTTGATAATATTACT 3050  
669 atacctcctcaaaagaaaggcgagccattcagacttccgatgcccttacc 718  
3051 ACAGCTAGTAACCCCCGGAGCCATTAATGTTCAAGGTCAAGGAAAAACCTT 3100  
719 attactggaaaccaaggggaaagtctttttctgacaa..... 756  
3101 AGGCATCTCAGGATTTCCTTATTTCATGTGCTTATTGTCCTCCAGGCA 3150  
757 .....tacttcttcggattctggagctgcaattttacagaag 794  
3151 CAACTGGTACGGAGCTATACTACAGACTAAAGGCAACACAACCTTAAAGAT 3200  
795 cctcggtgactatttctaataatgctaaagttcccttattgacaataag 844  
3201 AACTCTAGTCTTGTCTTCATAAAAACGCTCAACAGCAGAAGGGGGGGC 3250

845 gtcacaggagc gagctcctcaacaacggggatatgtcaggagggtctat 894  
 3251 TATCCAGTGTAAAGGAAGCAGTGATGCTGAATTAAAAATAGAAAATAATC 3300  
 895 ctgtgcttataaaacttagtacagatactaaggtcacccctcactggaaatc 944  
 3301 AGAATCTGGTTTCAGAAAACCTCCACTTCAAAAGGCAGGGCTATT 3350  
 945 agatgttactcttcagcaacaatacatcgacaacagcggaggagctatc 994  
 3351 TATGCTGATAAAACTCACCATGTCTCAGGTGGGCCTACATTATTTCTAA 3400  
 995 tatgtgaaaaagctcgaaactggctccggaggacttaccctattcagtag 1044  
 3401 CAACTCTGTATCCAACGGTTCATCCCCTAAAGGCGGAGCTATTAGCATAA 3450  
 1045 aaatagtgtcaatggaggtacagctcctaaaggtggagccatagctatcg 1094  
 3451 AAGATTCAAGTGGTGAATGTAGCCTAACCGCTGATCTGGAGATATTACC 3500  
 1095 aagat...agtgggaattgagtttatccggatagtggacattgtc 1141  
 3501 TTGATGGGAACAAAATCATCAAACAGGGAAATTACAAAGCTACGTGCTA 3550  
 1142 ttttaggaatacagtcaacttctactactcctgg.....gacgaatag 1185  
 3551 AAGAAATTCCATAGATCTCGGCACAGGGAAATTACAAAGCTACGTGCTA 3600  
 1186 aagtagtatcgacttaggaacgcgactgcaaagatgacagcttgcgttctg 1235  
 3601 AAGACGGCTTCGGAATTTCCTCTATGACCTATTACTGGGGAGGAT.. 3648  
 1236 ctgctggtagagccatctacttctatgatcccataactacaggatcatcc 1285  
 3649 .....CTGATGAACTAACATTAATAA.....AAAAGAAC 3679  
 1286 acaacagttacagatgtctaaaagttaatgagactccggcagattctgc 1335  
 3680 TGTTGATTATACAGGAAAGATCGTCTCTCAGGTGAAAAATTATCCGATG 3729  
 1336 actacaatatacagggAACATCATCTCACAGGAGAAAAGTTATCAGAGA 1385  
 3730 AAGAAAAAGCACGAGCGGAAACCTAGCTTCTACTTCACCAACCCATC 3779  
 1386 cagaggcccgagattctaaaaatcttacttcgaagctactacacgcctgta 1435  
 3780 ACATTATCAGCAGGATCTCTGTACTTAAAGATGGTGTATCTGTAACCGC 3829  
 1436 actctttcaggaggtaactctatcttaaaacatggagtgactctgcagac 1485  
 3830 AAAACAAGTAACGCAGGAAGCGGGATCTACCGTTGTATGGATCTAGGGA 3879  
 1486 tcaggcattcactcaacaggcagattctcgctctcgaaatggacgttagaa 1535  
 3880 CCACATTACAGACGCCTTCTTCAGGTGGAGAAACCATCACCTAACTAAT 3929

1536 ctactctaga.....acctgctgatactagcaccataaacaat 1573  
3930 CTAGATATTAAACATCGCCTCGTGGGGGGGGGGGTACCTCTCCTGC 3979  
1574 ttggtcattaaacatcagttctat.....agacggtgcaaagaaggc 1614  
3980 TAAACTCGAACAAATACAGCAAGTCAGCTATAACTAT...TAACGCTG 4026  
1615 aaaaatagaaaccaagctacgtcaaaaaatctgactttatctggaacca 1664  
4027 TCAATCTAGTCGATGCTGATGGCAATGCTTATGAAGATCCTATTCT... 4072  
1665 tcacttattggacccgacggcacgtttatgaaaatcatagtttaaga 1714  
4073 ..TGCTACGTCTAAACCTTTACAGCAATAGTAGCTACAACTAACGCTAG 4120  
1715 aatcctcagtcctacgacatcttagagctcaaagctctggaactgtaac 1764  
4121 TACAGTCACACAGCCTACAGATAATCTAACAAATTATGTCCCTCCTACTC 4170  
1765 aagcaccgcagtgactccagatcctataatgggtga.....gaaattcc 1808  
4171 ATTACGGTTACCAAGGAAATTGGACAGTAACTTGGGACACCGAACAGCT 4220  
1809 attacggctatcagggacttggggcccaattgtttggggacaggggct 1858  
4221 ACAAAAACAGCCACTCTAACCTGGAACAAACTGGCTACTCCCCTAACCC 4270  
1859 tctacgactgcaaccttcaactggactaaaactggctatattcctaattcc 1908  
4271 AGAACGTCAAGGACCTTAGTCCCAGAATACTCTTGGGTGCATTCTCTG 4320  
1909 cgagcgtatcggtcttttagtcctaatagcttatggaatgcatttag 1958  
4321 ACCTCAGAGCTATACAAAACCTAATGGATATTAGCGTCAATGGCGCTGAC 4370  
1959 atattagctctccattatcttatggagactgcaaacgaagggttgcag 2008  
4371 TACCATAGAGGTTTGGTATCCGGCTAGCTAACCTTACACAAAAG 4420  
2009 ggagaccgtgctttgggtgtggattatctaatcattttccataagga 2058  
4421 TGGCTCTGATACTAAACGCAAGTTCCGTACAATAGCGCCGGATACGCTT 4470  
2059 tagtacaaaaacacgacgcgggttgcgcattttagtggcggttatgtca 2108  
4471 TAGGCGTCTACGCAAAAACCTCTGATGATATTTCAGTGCAGCTTTC 4520  
2109 taggaggaaacctacatacttggtagataagattcttagtgctgcattt 2158  
4521 TGCCAACTCTCGGAAAGGACAAAGACTATTTAGTGTGAAAAACACGC 4570  
2159 tgcgtacgtttggaaagagatagagactactttagtgcatttgcattt 2208  
4571 CAACATTTACGCAGGTTCTCTATTATCAGCATATCTCCTATTGGAGCG 4620  
2209 tacagtctacqqaaggaaactctctattaccacqacaacqaaacctatatct 2258

4621 CTTGGCAGAACATCTGCTACAAAACACTATCGGTGCAGAAGCTCCGTAGTC 4670  
|| | || | || | | | | | | | | | | | | | | | |  
2259 ctcttccttgc当地actacggccttgc当地gtcttatgttcc当地acagag 2308  
  
4671 CTTAACGCACAGTTAACCTATTGTCATGCTCAAACGACATGAAAACCAA 4720  
| | | | | | | | | | | | | | | | | | | | | |  
2309 attcctgttctttcaggaaaccttagctacacccatacgataacga 2358  
  
4721 CATGACGACTACTTACGCTCCTCGTAAAACAACGTATGCAGAAATCAAGG 4770  
| | | | | | | | | | | | | | | | | | | | | |  
2359 tctgaaaaccaagt.....atacaacatatacctactgtttaag 2396  
  
4771 GTGATTGGGGTAACGATTGTTCGGAGTCGAGCTTGGTGCAACTGTGCCT 4820  
| | | | | | | | | | | | | | | | | | | | | |  
2397 gaagctggggaaatgatagtttc当地ctt当地agaattc当地ggtaagagctccg 2446  
  
4821 ATCCAAACAGAACATCTCTCCTATTGATATGTAACACCTTCTGAA 4870  
| | | | | | | | | | | | | | | | | | | | | |  
2447 atttgcttagatgaaagtgc当地tattt当地gagc当地gatgc当地ccctt当地catgaa 2496  
  
4871 GTTTCAACTTGTGCATACGCACCAAGATGACTTAAGGAAAACAATAGCG 4920  
| | | | | | | | | | | | | | | | | | | | | |  
2497 attgc当地gtt当地gtc当地cacatc当地aggaaagg当地tttaa当地agaacaggaaacag 2546  
  
4921 ATCAGGGAAAGATACTTCGAAAGCAGCAATCTCACCAACCTTCTGCCT 4970  
| | | | | | | | | | | | | | | | | | | | | |  
2547 ...aagctc当地gtgatattt当地gaaaggtagcc当地gtt当地gtgatattt当地gc当地ctt当地acc 2593  
  
4971 ATCGGCATCAAGTTGAGAGATTGCTAACAAACGATAACAGCTTCTTATCA 5020  
| | | | | | | | | | | | | | | | | | | | | |  
2594 atcgggatccgattt当地gataaggaaatcagactgcca当地agatgcaacgtacaa 2643  
  
5021 TGTCACTGCTGCTTATTCTCCTGATATCGTAAGAAGTAACCCCTGACTGTA 5070  
| | | | | | | | | | | | | | | | | | | | | |  
2644 tctaactctt当地gg当地tatactgtggatctt当地gtc当地tagtaacc当地ccgactgta 2693  
  
5071 CTACTTCTCTGTTAGTAAGCCCCGACTCTGCTGTCTGGTAACGAAAGCC 5120  
| | | | | | | | | | | | | | | | | | | | | |  
2694 cgacaacactgcaatttagc当地gg当地tattct.....tggaaaacctt当地cggt 2737  
  
5121 AACAAACCTTGCAGAACGCGCTTCATGCTACAAGCAGGAAACTACTTGTC 5170  
| | | | | | | | | | | | | | | | | | | | | |  
2738 acgaattt当地gg当地caagacaagctt当地tagtc当地ctt当地cggtc当地aggaaaccattttg 2787  
  
5171 TTAAAGTCACAACATAGAAATCTCAGCCAGTTCGGTTTCGAGCTCAGGG 5220  
| | | | | | | | | | | | | | | | | | | | | |  
2788 cttaactcaaattt当地gaagc当地ctt当地tagcc当地attt当地ctt当地gaattt当地gc当地gt 2837  
  
5221 GATCTTCACGAACCTATAACGTAGATCTCGGATCGAAGATCCAGITCTAA 5270  
| | | | | | | | | | | | | | | | | | | | | |  
2838 ggtcatctc当地gcaattacaatgttagacttagggagcaaaatccaattctaa 2887  
  
5271 TCTCATCCACCTCTCCTACCCCCGTTCCCACGGGGTAGGGCCTTATAACCT 5320  
| | | | | | | | | | | | | | | | | | | | | |  
2888 t.gcgtagctt当地gg当地taaagagactcc当地atcatc当地gaaaggaaaagagctt 2936

5321 TGACTCTCCTGGAAATATCCCCAACAAAGAGTCAAAAAAAATACGTCTCAT 5370  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
2937 taagatttcttcaaqqcttttcgatttcgatttcattttaatgtttttt 2986

5371 AGGATTCTGGTCTATTCCTTTCTTATTTGGAGAAAAATCTGATCAC 5420  
| | |  
2987 qctaaaacacttcc..... 3000

### **Alignment 3**

GAP of: pomp90.pep check: 1153 from: 1 to: 839

WPDEF            prt  
pomp90    prt

to: 396prt.pep check: 2118 from: 1 to: 928

WPDEF  
396prt

Symbol comparison table: /big1/gcg/gcgcore/data/rundata/blosum62.cmp  
CompCheck: 6430

### BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Gap Weight: -8 Average Match: 2.912  
Length Weight: 2 Average Mismatch: -2.003

Quality: 1485 Length: 958  
Ratio: 1.770 Gaps: 29  
Percent Similarity: 54.512 Percent Identity: 47.960

Match display thresholds for the alignment(s) :

| = IDENTITY  
: = 2  
. = 1

pomp90.pep x 396prt.pep March 2, 2001 16:59 ..

```

1 MKHPVYWFLISSLFASNSLSFANDAQTALTPSDSYNGNVTSEEFQVKET 50
|| | . | . || || :| | | | :. || . | | :|. .
1 mkssfpkfvfst faifpnlsmi atetylldssasfdgn knqnfsvres 46

```

51 ..SSGTTYTCEGNVCI.SFAGKDGLKKSCFSAT.DNLTFLGNGYTLCFD 96  
.....||||| .||| : . | . : |||||. | .||| |||| .| |  
47 qedaqttylfkqnvttlenipqgtqtaikscfnntkadlftangansilfg 96

144 GNTTLKDNNSSLVFHKNCST..... AEG 165  
| . . | | |||. | | | | | | . |  
147 gsslstknvslifsknfstdnggaitaktlsltattmsalfsentsskkq 196

166 GAIQ.....	169
167 gaistadtitanusconfundens.....	511-516

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247 nkvtgasssttgdmsggaicayktstdkvtltgnqmlifsnntsttagg 296

199 AIYADKLTIVSGGPTLFSNNSVNSNGSSPKGGAIISIKDSSGECSLTADLGD 248  
|| | : ||| |||. . . |||||. . | ||| ||.|| |  
297 aiyvkklelasggltlfsrnsvnggtapkggiaied.sgelslsadsgd 345  
  
249 ITFDGNKIIKTSIGGSSTVTRNSIDLGT.GKFTKLRAKGFGIFFYDPITG 297  
| | | : . .. . |.||||| | | |||. | | : |||||  
346 ivflgntvtsttppgtn...rssidlgtsakmtalrsaagraiyfydpitt 392  
  
298 GGS....DELNINK...KETVDYTGKIVFSGEKLSDEEKARAENLASTFN 340  
| | | | | : . . . | | | | : . | | . | | | |  
393 gssttvtdvlkvnetpadsalqytniiftgeklsseteaadsknltksll 442  
  
341 QPITLSAGSLVLKDGVSVTAKQVTQEAGSTVVMDLGTTLQTPSSGGGETIT 390  
| : | | | . | | | | . | | : | . | | . | | : | . : | |  
443 qptlsggtlslkhgvtlqtqaftqqadsrlemdvgttle.pa...dtst 488  
  
391 LTNLDINIASLGGGGTSPAKLATNTASQAITIN.AVNLDADGNAYEDP 439  
: | | | . : | | | : | . : | . : | | . | | | |  
489 innlvinissi...dgakkakietkatsknltsgtitlldptgtfyenh 535  
  
440 ILATSKPFTAI...VATTNASTVTQPTDNLTNYVPPTHYGYQGNW.TVTW 485  
| . : : . | | | | | : | | | | | : | | | | | : |  
536 slrnnpqsydilelkasgtvtstavtp.dpimg..ekfhygyqgtwgpiwv 582  
  
486 DTETATKTATLTWEQTGYSPNPERQGPLVPNTLWGAFSDLRAIQNLMDIS 535  
| . | | | | . | | | | | | | | | | | | | | | : . | | : .  
583 gtgast.tatfnwtktgyipnperigslvpnslnafidisslhylmeta 631  
  
536 VNGADYHRGFVWVSGLANFLHKSGSDTKRKFRHNSAGYALGVYAKTPSDDI 585  
| | | | . | | | | . | : | | | | | | : | | | | |  
632 neglqgdrafwcaglsnffhkdstktrrgfrhlsuggyvigglnhtcsdk 681  
  
586 FSAAFCQLFGKDYLVSKNANIIYAGSLYYQH...ISYWSAWQNLLQN 631  
| | | | : | | | | . | : | . | | | | | | | | | | |  
682 lsaafcqlfgdrdyfvaknqgtvyyggtlyyqhnetyislpcklrpcsls 731  
  
632 TIGAEAPLVNQLTYCHASNNDMKTNMNTTYAPRKTTYAEIKGDWNDCF 681  
: | | ... | . | | | | : | | | | | | | | | | | | |  
732 yvpteipvlfsgnlsyhtndlkt.....kyttyptvksgwgnndsf 773  
  
682 GVELGATVPIQTESSLFLDMYSPFLKFQLVHTHQDDFKENNNSDQGRYFES 731  
. | | | | : | | | : | | | | | | | | | | | | | | |  
774 alefggrapicldesalfeqympfmklqfvyahqegfkeqgt.earefgs 822  
  
732 SNLTNLSLPIGIKFERFANNDTASYHVTAAYSVDIVRSNPDCSTSLLVSP 781  
| | | | . | | | | : | : . | . | | | | | | | | | | | |  
823 srlvnlnalpigirfdkesdcqdatynltlgytvdlvrsnpdcttlrisg 872  
  
782 DSAVWVTKANNLARSAFMLQAGNYLSSLSHNIEIFSQFGFELRGSSRTYNV 831  
| | | | | | | | . | . | | | | | | | | | | | | | | | |  
873 ds..wktfgtnlarqalvragnhfcfnnsfeafsqfsfelrgssrnynv 920  
  
832 DLGSKIQF 839  
| | . | | |  
921 dlqakyqf 928

## Alignment 4

GAP of: pomp91.pep check: 2232 from: 1 to: 847

WPDEF prt  
pomp91 prt

to: 396prt.pep check: 2118 from: 1 to: 928

WPDEF  
396prt

Symbol comparison table: /big1/gcg/gcgcore/data/rundata/blosum62.cmp  
CompCheck: 6430

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl. Acad.  
Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.912  
Length Weight: 2 Average Mismatch: -2.003

Quality: 1468 Length: 967  
Ratio: 1.733 Gaps: 29  
Percent Similarity: 51.238 Percent Identity: 44.059

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 2  
. = 1

pomp91.pep x 396prt.pep March 2, 2001 17:01 ...

1 .....MKHPVYWFLISS 12  
51 gttylfkgnvtlenipgtgtaitkscfnntkgdltftgngnsllfqtvda 100  
13 SLIVSNSLYSEEPDQKTLTSAHSYNGNTNSEP FNPLSTSNSNGTIYTCTG 62  
101 gtvagaavnssvvdksttfigfs.slsfiaspgssitt..gkgavscstg 147  
63 NICIAYAGLDGSGLSSSCF.TD.....TAGNLSFLGNGYTLCFDNITTQS 106  
148 slslt...knvslifsknfstdnggaitaktlsltgttmsalfse.ntss 193  
107 SHPGAI SVSGTNKTL DISGFSLFSCAYC PPGATGYG.AIKAVGNTTIKDN 155  
194 kkggaiq...tsdaltitg.nqgevsfsdntssdsgaai fteasvtisnn 239  
156 SSLVFHKNCSTG.....EGGAIQCKASSSEAE LKIENNQNLVFAEN 196  
240 akvsfidnkvtgasssttgdmsggaicayktstdkvltgnqmqllfsnn 289

